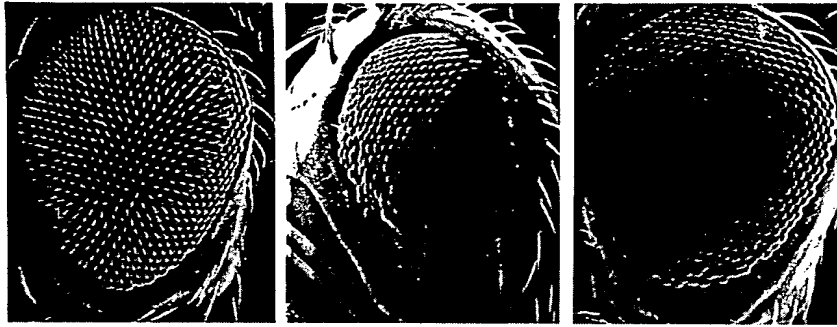


Figure 1

A



wild type

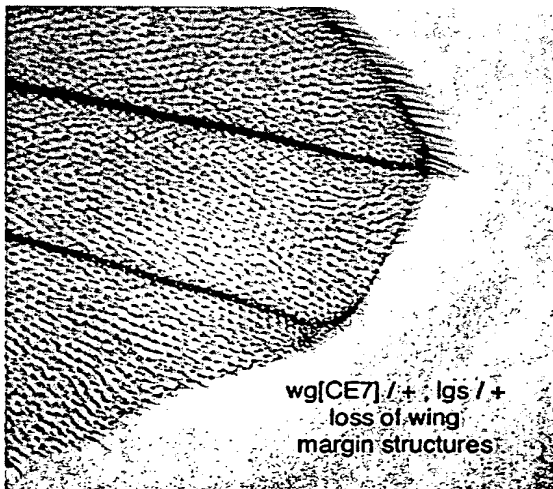
sev-wg

sev-wg, $lgs^{S17}/+$

B



C



$wg[CE7]/+; lgs/+$
loss of wing
margin structures



$wg[IL114]/+; lgs/+$
Janus phenotype (double dorsal)

Figure 2

ACGAGTGCCTCTCTTATTATGCGAGCTGTTATTCCTCAAAAGTATGTTTCGCAATTTTCGACT	60	CGCGCCTAGCAACTCTTTTTCGACCACTGCTGATCTCTATGCGCAACGAACTGAATTGA	3060
CCTGCTAACATAAGCAGACGTTTAAAGCAGGAACTTTGGGCTATAGGCCCCAAAATTTCA	120	APSNNSFVDQSDPMMGNETELM	445
TTAGCTTAATACGATGCTCGGAAGTGTATTCGATTTGCAATATACATAAAATTTGTGAC	180	TGTCTGGGAAGCGGATCTCTCAAAACACGATAGGTCTGGACAAAATCTACGAAATCATG	3120
ATAGAATAGGAGAAATCCACATACAAATACAAAAATACAAAAATCCCTCCAGTAAAAATTTAA	240	CWEGGGSSTNTSRSSGQNSRNHHV	465
AACGATATCGTGTGTTTCTCTGCGTATCTCAGGTGAGATGTAAATGCGATGCAATAGAGTG	300	TAGCAGTATCAGTACATCCAGCGAGTCAAGGCAATAAAGATCTCGAAAGCAGCTGGCG	3180
GTGAGTGCTCGCTGCGATCTCTGCTCTAAATATGCTTAATTTGCGTTCGCGGACCTCAAA	360	DISISTSSSESQAIKILEAAGV	485
AGCAATAAAACGATGATTTTAAATTCCTACTTGAAGCAATTAGCCACACAAAGGATCTTGG	420	TTGATTTGGGACAGGTACAAAAAGGAAGGATCTCTGGCTGACAACTGAAACAAACATTTG	3240
GAAAGTGTGATTTGAAGAAATTCGATTTCTAGATGCTCTCGACAAATGCCCCGAGTC	480	D L G Q V T K G S D P G L T T E N N I V	505
	5	TATCACTGCAAGAGGTAAAGTTCCAGACGAAAACTTACACCAACACAGCGGCAACATC	3300
CAACCCACAAACAGCGCCAAACAACTCCGATGCTCTCTCAACAGTGCTATCTGATCAA	540	S L Q G V K V P D S N L T P Q R Q H R	525
T Q Q Q P P P N S D A S S T S A S G S N	25	GGAAGAACAGTTGGCAAAAAATAAAAAATGAATCAATTTCTTTTCTGAAAAATGAGA	3360
ATCTCGAGCAGGATGCGAAATGGGAGCTGGCGGCGAGCAGAGTTCTTCGGAAGACCC	600	E E Q L A K I K K M N Q F L F P E N E N	545
P G A A I G N D S A A S R S S P K T L	45	ATTCACTAGGAGCTAATTTAAAGCTCAGATTAACAAAAATTCAGAGGATTTAATGATGG	3420
TTAATAGCGAAACCTTTTCTACTTTTGTCCCGGTAAGACTTGTATTTGATTTCTTTT	660	S V G A N V S S Q I T K I P G D L M M G	565
N S E P F S T L S P	55	GGATGTCTGGGTGCGGAGGCGGATCTATTATAATTCAGGATTCGCAACATGCTATGCT	3480
CCGGAATTAACAACTTTCTGTGTTTCCAGATCAAAATAAAATGACGCGAGAAAGGCG	720	M S G G G G G S I I N P T M R Q L H M P	585
D Q I K L T P E E G	65	CAGGTAAACGCAAAATTCGAGCTCTTATTCGCGCAAACTTCAGGACTTCGCGAAGATGTAA	3540
ACTGAGAAAGAGCTACTCAACTAGTGAATAAGCTGCCACTTGAAGAGCGCCAGGAGT	780	G N A K S E L L S A T S S G S E D V M	605
T E K S G L S T S D K A A T G G A P G S	85	TTCACTCCAGGAGATTTATATCAGATATGCGGTACCGGTAAATAGGATTAATATCAAA	3600
GGAAATTAATCTCGCGGAGGACAAACTATGCTAAGCGAGAACTCTCAGACGACAAATCAAC	840	H P G D V I S D M G A V I G C N N N Q	625
G N N L L P E G Q T M L R Q N S T S T I N	105	AAACCAAGTTGCAATGTGATCTGAGTGGTGTGTTCTCACTGGAACCACTCCAGCTGGAG	3660
TCGTGCTAGTGTCTCTCCACAAATCCAGTGAACACTCGAATAGCAGCAATGTGTCT	900	T S V Q C G S G V G V V T G T T A A G V	645
S C L V A S P Q N S S E H S N S S N V S	125	TAAATGTCAATATGCAATTTGCTCAAGCTCCGCGCGCCGAAATGGAATATGATGGAAGCT	3720
GCTCAGCTGGGCTTACTCAGATGCTGATGATGATGATGATGATGATGATGATGATGATGAT	960	N V N M H C S S S G A P N G N M M G S S	665
A T V G L T Q M V D C D E Q S K K N K C	145	CTACGATATGCTAGCTGCTGTTTGGCAACCAAGCTCATCGAAGCTTCGGAAGCGCCAG	3780
AOTGTGAAGCAGGAGGCTGTGAAGACTGCGCTCAAAATGGTTTAAAAATTTAAAAATG	1020	T D M L A S F G N T S C N V I G T A P D	685
S V K D E E A	152	ATATGCTTAAGAAAGTTTAAATCAAGATAGCGGAAACCCATTCACATCAAGGGGAGTG	3840
TATTTGGGCTTCACTTTGTTAATCATTTAATTTGTTTTTTTTTTTCTATACATTTT	1080	H S K E V L N Q D S R T H S H G G V A	705
AGTTTAAATCTGTAATCTGTAATCTGTAATCTGTAATCTGTAATCTGTAATCTGTAATCT	1140	CTCAATGTGAGTGTGGAAGATTAACATCAATTTTTCGAAAGAACCCCTCAAGGGGGGCA	3900
TTGGAAACCTGTAATTAAGCTCATATAAATAATTAATTAATTAATTAATTAATTAATTAAT	1200	M E M S K I Q H Q F F E R L K G G K	725
ATGTACTCAACATCTCAAGAAAGAGCTCAAAATTTGATCACTAATTTAGTTTGAAGAAA	1260	AGCCGACAGCAAGTCACTGGAACTGTATGATCAACAGCAAGAACCCCTCTGATCTGGTG	3960
ATTGCTGTACTTTTGAAGATATATTAATTTAAAAATTTTCTGTAAGTGAATGATATAATAG	1320	P R Q V T G T V V P Q Q T S G S G G	745
TCACAAATTAATTTTGTAGTAACTGCTAAGCAATTTTGAATAGCGGTGCTACGAGATGCT	1380	GAAACTGTTAAACCAACAGGTGCGACCCCTGCAAGGTCCACCTCTCTTACCCTCCA	4020
ACTAGACGCGGTGTAAAGCTTAATTTTATTTTAAAGCTGCTCTAATTTTCATTAACCAT	1440	N S L N N Q V R P L Q G P P P P Y H S I	765
TAATGTGCTTCTCAGAAATAAGGTCTAATAAGCAAAAGGTCAAGCAGCTGTTGCGCGC	1500	TCGACAGATCTGCTCAATCAATAGCACTCAATTCGCGCAATTCGCTGAGTCCAAAC	4080
E I S S N K A K G Q A A G G G	167	Q R S A S V P I A T Q S P N P S S P N N	785
TCGCAACAGGTCTTACATCCAGTTGACTGTCTCAAGGAAGAACCCAGATGTCTTAGGC	1560	ATCTATCTCTCCCTCAGCGGCAACCGCAGCAGCTATGGGATTTGCGGACCACTCTC	4140
C E T G S T S S L T V K E E P T D V L G	187	L S L P S P R T T A A V M G L P T N S P	805
AGTTTAGTAAATATGAAAAAGAAAGAAAGAAATCAATTCGCGCAAGATGTCCTGCTT	1620	CTAGCATGGATGGAAACAGGATCATTTCTTATCTGTTCCGCAAGCTAATCTTCGAGC	4200
S L V N M K K E E R E N S P T M S P V	207	M D G T G S L S G S V P A G T S T V	825
GGTTTGTGTTCAATTTGTTAATGACACAGGCAACTCCGCTACACCGGTAAGTTTAAAGAG	1680	TTCAAGGACGCAACCAACAGTCTCTCAGCAACCAAGAACTGTTTTCAGGACGACCC	4260
G F G S I G N A Q D N S A T P	222	Q A G T T T V L S A N K N C F Q A D T P	845
ATCCATATAAGCAATAACAGAAATTAATGTGCTAGTACCAATTTTATTTGATAGTCAAA	1740	CATCGGCTCAAAATCAAAATGCTAGTGAATAACCGGATTCGTAAGCGTTCTTACGATA	4320
GAACTACTATAGGATATCTCTGCGCTTTTAAATTTTATTTTAAATTTAGGAAATAGCAATAT	1800	S P S N Q N R S R N T G T S S V L T H N	865
TTCTAATTTTGAATAAAATTTGATTAATTTAATAGATTAATTTAAAAACCTTTTGAATTAG	1860	ACTTAAAGCAGCAACCCAGTACCCCTTATCTCACTCTATCCCAAGGAATTTGAGTCT	4380
ACATACCTTTCAAAAAATCAGTAATCTGGAACGAGAGTGTGCTCCGGAAGGAGACTA	1920	L S S N P S T P L S H L S P K E F E S F	885
CTATAAAACCTTTTGTAGCTATCTGATAGTCTCAGCTACTAAAAATGATTAGTTTAGAAA	1980	TCGCTGCTCTCTGCTGTTATGTTATATTTGTTTAAATTTTAAAGCAAAATCAAAAT	4440
ATGCTGTAAATTTTGTAGGAAGTTTCTATTTAGAAGAAATGTGATTATTTTATTAACCC	2040	G Q S S A	890
CCTTCAGGCGAATACATTTGTTTCTAGATATTTTGAAGAAACAAATGTTAAGTTGGA	2100	TGAATTTGCTTAAATAAGTTTATATTTATCATTAACCTGGAAAATTTGATGAAAAATCA	4500
AAGTGCTATATAACAGAAATTCACAGGTTTCAAAATCTAACAGGTTTGTGATTTAAATTT	2160	GGAAATAGAAAAATAAATATTTTTCGCGACCGCCCATCCATTTCTTGAATCCAAATTTCT	4560
TGAATTAATGAGAAATTAATCACTCTAGTTAAATGTTTAAATGCGATTAAGGTGGACA	2220	GAGTGATTGTTAGAGATAATCTACTATTTAAATTTAAACAGGAAAAATTCATATCTGTTAAT	4620
ATCAGACAGATTTTCAATTTTGTGCTGTATATAGAAAGTCCGCTTCACTCTCTCTGCG	2280	TGAABATCACTATTTGTTTAAAGAAATTTAAAAATGTTTATTAATAATTTTCTACAG	4680
CGGCTTCACTACTAGTGTGAGGTTCGCGCGCAGTGTATTTATATAGATGATTTACGAGTTA	2340	G	891
TTTAAATTTTATGTTGTTATTTTAAATAATATCTTATTTATTCATTTTACATAGTTAAAA	2400	TGATAACATGAAAAATAGCGGACCAAGCCCAAGGCTCAGCGGTCAAGCTTAATAGTCT	4740
	225	D N M K S R R P S P Q G O R S P V N S L	911
TTGAAAGAAATTTCAACGACAGTACCAACGAAAAAAGAGATCGTCTCTGACAAATGAATA	2460	AATAGAGGCAATAAAGATGATACGATTTCTGCTGCTCCAGCTCTGTTTAAACCCGATCC	4800
E R I S N D S T E K K G S S L T H N N	245	I E A N K D V R F A S S P G F N P H P	931
ATGACGAAATGAGCATGGAAGCTGCAATCAGTTGAAATCCGATTTTATCAATGAATCTT	2520	ACATATGCAAGCAATTCAAATTCAGCATTAACAGGCTTAATAATGCGCTTACCAATAT	4860
D E M S H E G C N Q L N P D F I N E S L	265	H M Q S N S N S A L N A Y K M G S T N I	951
TAAATTAATCTGCAATTTTGAAGCATATAGTGAAGCGAGTAGGACCAATACCGGAAATCG	2580	ACAGATGGAAGTAAATATTTAAATATTTTATTTAAGGTTTTTGTGTTAATTTATCTCTCT	4920
N N P A I S S I L V S G V G P I P G I G	285	Q M E	954
GAGTTGAGCGGAGCGGAAATTTTATGATGCAACGCAATGGAATCTCTCTGCGGAT	2640	TTTCAAGCTCAAGCATCAGCGCAAGGTGATTCGTTACAAATTTAGTCGGCGCTCCGATAAT	4980
V G A G T G N L L T A N A N G I S S G S	305	R Q A S A Q G G S V Q F S R R D N	972
CGATTAATTTTGAATTAATCAACAGCAAGTACATATTTCTGTTTCAACTCAGC	2700	ATTCTGCTAAATCCCAATAGTGGCAATCTCTTCCACCAACAGATGACCCCAAAATCTC	5040
S N C L D Y M Q Q N H I F V F S T Q L	325	I P L N P N S G N R P P N K M T Q N F	992
TGCGCAACAAAGGGGCGAATCAGTTTGAAGCGGTCAATTTCAACTATTTATTCGATCT	2760	GATCCAACTCTCTCTTTGGCAGAAAATGTCGCAACAACTAACAAAGTGTGCTCAGCATG	5100
A N K G A E S V L S G Q F Q T I I A Y H	345	D P I S S L A Q M S Q Q L T S C V S S M	1012
ACTGCACTCAGCTGCTACAAAAGCTCTCTGGAAGACTTTTATGAAAAACCTTTTAA	2820	GGTAGTCCAGCGGAACTGTTGTTATGACGATGATGGGGGTCGCGGACGCTCCGACATC	5160
C T Q P A T K S F L E D F P M K N P L K	365	G S P A G T G G M T M M G G P G P S D I	1032
AGATTAACAAAGTTACAGCGGCAACATTCGCTGCGATGCGCATGATAGGCAATGCGGCAAG	2880	AATATGAGCATGGAATAATTTCCGAGCTAGATGATGGAATGGAATAGATACCAATTAACAA	5220
I N K L Q R H N S V G M P W I G M G Q V	385	N I E H G I I S G L D G S G I D T I N Q	1052
TTGACTTAATCTCTCTTATCTGCTAGCGGAAATAACACAAACAGCGGCAATACAAAG	2940	AATACTGATCTCAATGAATGCTGTAATGAATCAATGGGTCGCGGAAATGCTGAATCT	5280
G L T P P N P V A K I T Q Q Q P H T K T	405	N N C H S M N V M N S G P R H L N P	1072
CCGTAGCGCTATGGAAGCCCAATTCATCAACATGAAGACGAAAGCTACTGTTAA	3000	AAAATGCTGCTAGCAGCGGCTCAAAATGGAACCGCTGCTTTAATCTGTAATTTCCCAAT	5340
V G L L K P P F N Q H E N S K R S T V S	425	K M C V A G G P N G P P G F N P N S P	1092
		GGTGGATTAAAGAGAAATTCATAGGCTCTGCTGCTGCTCAGCAAACTCTTCAAACTTT	5400
		G G L R E N S I G S G C G S A N S S N F	1112
		CAAGGGTGTGTTCCACCTGTGCGGAAATGATGGGTGGAATGCGAATCAATTTTGGTTGG	5460
		Q G V V P P P G A R M M G R M P V N F G S	1132
		AAATTCATTCGAAATTTCAAGTAAAGGCGGATCCCAACCAACATGGAATCAATACATGCA	5520
		N F N P N I Q V K A S T P N T I Q Y M P	1152
		GTAAGGCGAGAACCCCAACAAATAACAAACATGGAATTAATTTGGAATGCGCA	5580
		V R A Q N A N N N M G A N N V R M P	1172
		CCTAGCTGGAATTTTTCGAGAGTACCGTAAACCTCAAAATGCGGTGCTGATAGGCAATGG	5640
		P S L E F L Q R Y A N P G V N F G N G	1192
		TCGCCAATGCGCCCACTCAGCGGAGCGGATCTCTGCTGGAATGCGGATTTGATGGG	5700
		S P I C P P S A S D G T P G M P L G A	1212
		GGACCAAGGCGCGAGGATGCTAATGAATTTCTCCGAGACCAACCAAGCAAGATC	5760

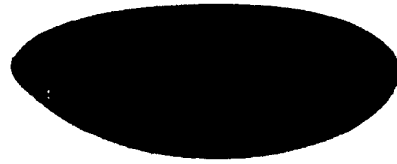
Figure 2: *legless*

```

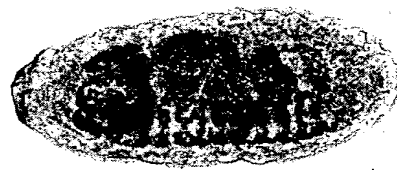
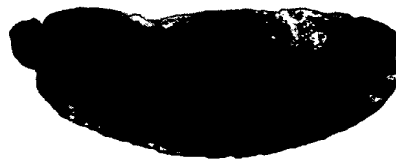
G P G A G G M L M N S S G E Q H Q N K I 1232
ACAAACAAATCTGGGGCAAGCAAATGGTATTAACTTCTTTACAGAAATGCAATCAAAATGTCT 5820
T N N P G A S N G I N F F Q N C N Q M S 1252
ATTGTTGACGAAGAGGTGGATTACCCGCCATGACCGATCAAATGAATATTGGTCAACCA 5880
I V D E E G G L P G H D G S M N I G Q P 1272
TCTATGATAGGGGCAATGCTCCACATGCCATGCCGCCAAATGTAAATGGTGGCGGATG 5940
S M I R G M R P H A M R P N V M G A R M 1292
CCACCCGTAAACAGGCAAAATTCAGTTTGCACAGTCATCGGATGGTATTGACTGTGTGGG 6000
P P V N R Q I Q F A Q S S D G I D C V G 1312
GATCCGTCACTATTTTCACTAACGCTTCTGCAACAGCGCTGGACCAACACATTTTGA 6060
D P S S F F T N A S C N S A G P H M F G 1332
TCAGCACAAAGGCCAATCAGCCTAAGACACAACATAAAGAACATACCTAGTGAATG 6120
S A Q Q A N Q P K T Q H I K N I P S G M 1352
TGTCAAAACCAATCGGGACTTGCAGTGGCACAAGGGCAGATCCAACTGCATGGGCAAGG 6180
C Q N Q S G L A V A Q G Q I Q L H G Q G 1372
CATGCCAGGGTCAGTCTTTAAATGGACCTACTAATAATAATTTAAATGCAATGCCGGA 6240
H A Q G Q S L I G P T N N N L M S T A G 1392
AGTGTGAGTCTACTAAAGGTGTCTTGGCATCAATTTGGTAGTCCCTCTTCTACGGAC 6300
S V S A T N G V S G I N F V G P S S T D 1412
CTGAAGTATGCCAGCAATATCATAGTTTTCAGCAGCAGTTATATGCTACCAACACAGG 6360
L K Y A Q Q Y H S F Q Q Q L Y A T N T R 1432
AGTCAACAAACAGCATATGCCACGAGCAGCAGCAACATGATAACAAATGCCGCG 6420
S Q Q Q Q H M H Q Q H Q S N M I T M P P 1452
AATTTATCAACAAATCCAAAGTTCTTTTGTCAACAAATAAACTTCTAAATTTTGGCGCC 6480
N L S P N P T F F V N K * 1465
TGTCAATGATTTGTTTACTAGTCTCCAAATTAAGACATGCAATCTCTAAATAAGATTTTTT 6540
GAAAGTTATTTACTTAGGTGTTTTTACAAACGAGAAAAATAAACTTTTGGATATGCAAAATG 6600
ATAACGTTGGAAACAACTAATTCATTTTGCACTTTTAGAAGTCACGTGAAAGTTAAATG 6660
TAGAATCTGTATTTTAAACATAATAGTCAATCTGTAAAAATAATTAACATCGAAATTTTA 6720
GTTATCAGCAGCTATTTTCTGTATTATTTAATATGTGGCGTGTCTCTCTGTGTAAAT 6780
GAAATTAATAATATATATATAATGTAAAAAGCTATTGATATATATGCTCTCAACTGTAT 6840
TGTAATCAATATTAAGAGAACTGTAAATTCCTCCATATAAAGGTAAATGAAAAAAAAAAAA 6900
AAAAAAAAA 6909
    
```

Figure 3

A



yw x lgs anti-sense



yw x lgs sense



B

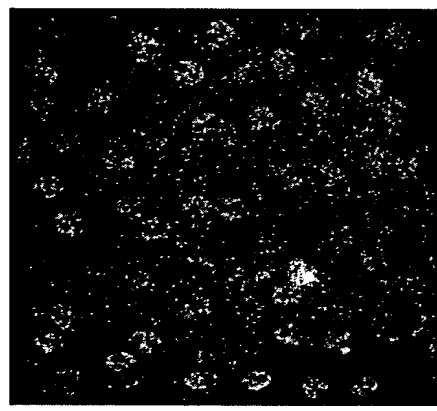
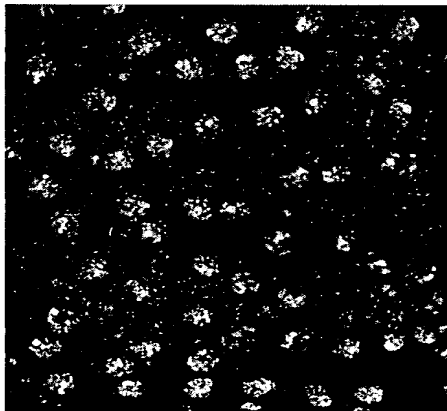


Figure 4

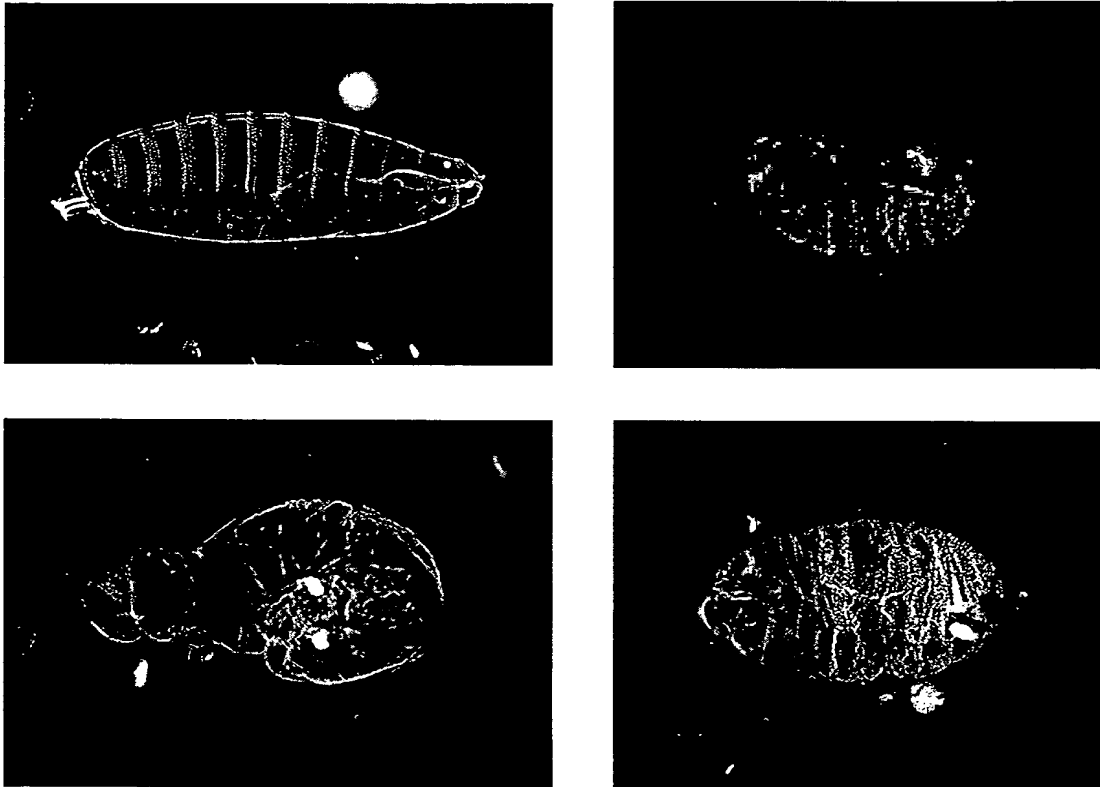
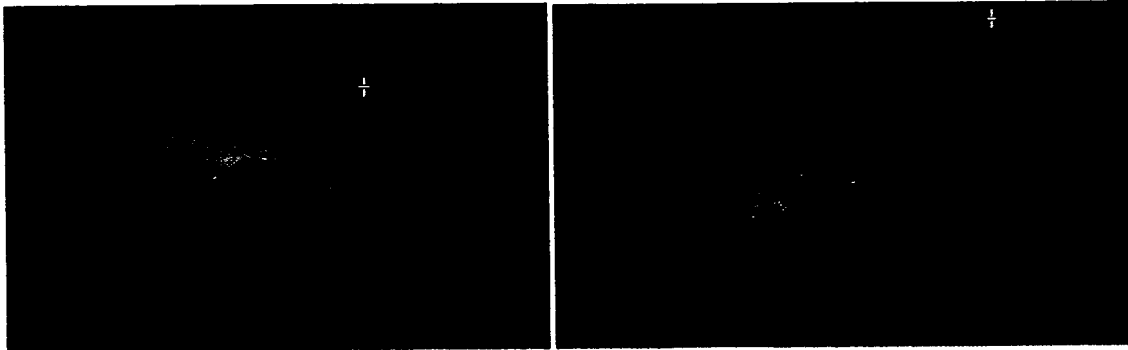


Figure 5

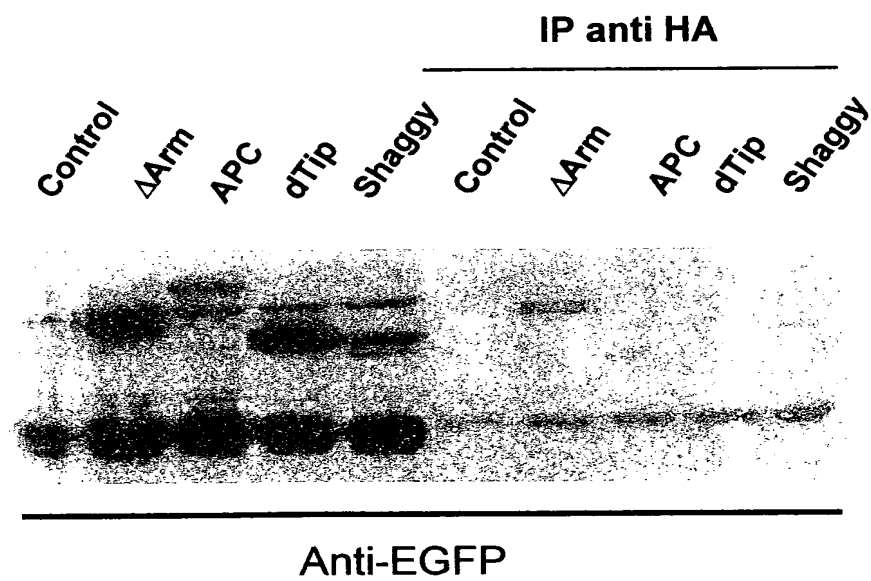
A

EGFP-Lgs

EGFP-Lgs + pcDNA3-Arm-NLS



B

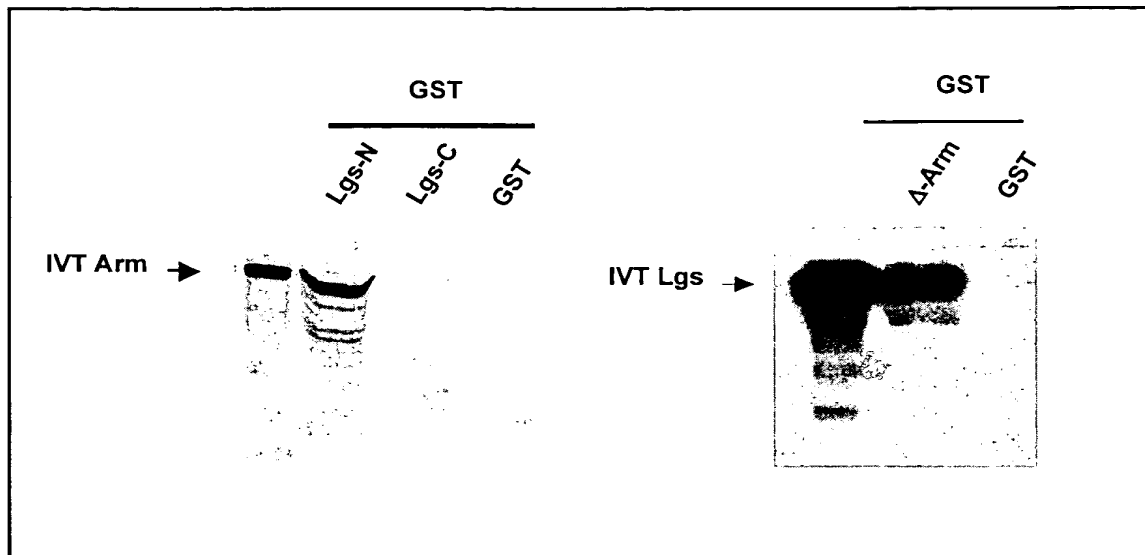


5C

		BAIT fusions: pLex						
		Lgs 1-1464	BCL9 199-392	BCL9 1-1426	Dco+	Δ ArmC	$\Delta\beta$ -Cat	Pan
PREY fusions: pJG4-5	lgs364-555					+		
	lgs1-385					-		
	lgs1-732					+		
	lgs364-1090					+		
	lgs726-1464					-		
	lgs1-1464				-	+	n.d.	+
	BCL9 199-392					+	n.d.	
	BCL91-1426					+	+	
	Dco+	-						
	DAxin	(+)				+		
	Δ ArmC	+	+	+				+
	β -Cat	+	+	+				
	Pan	+				+		
	pJG4-5	-	-	-		-	-	

+: interaction seen in yeast two-hybrid assay
 -: no interaction seen in yeast two-hybrid assay
 n.d.: not done
 numberings refer to amino acid positions.

5D



5E

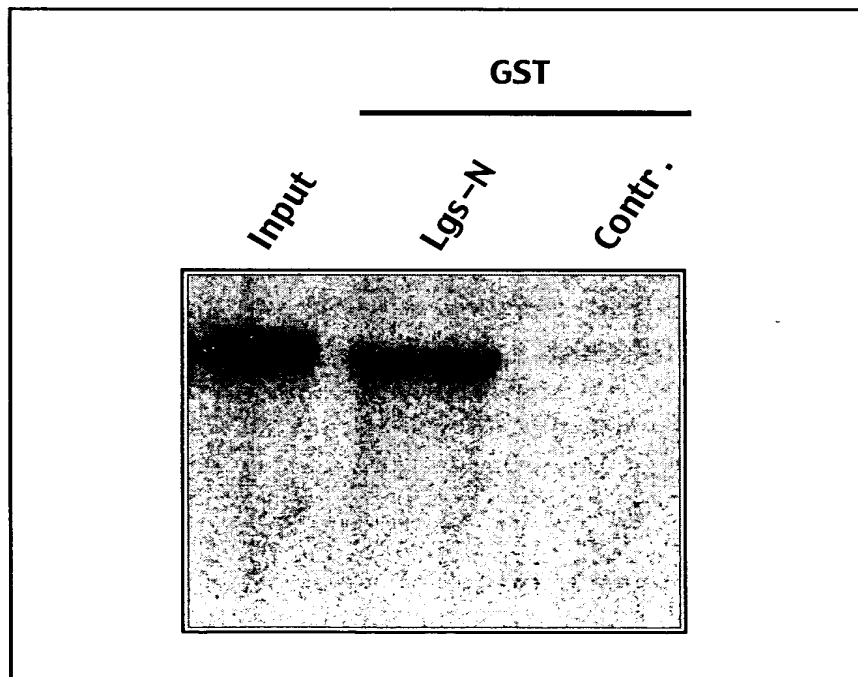


Figure 6

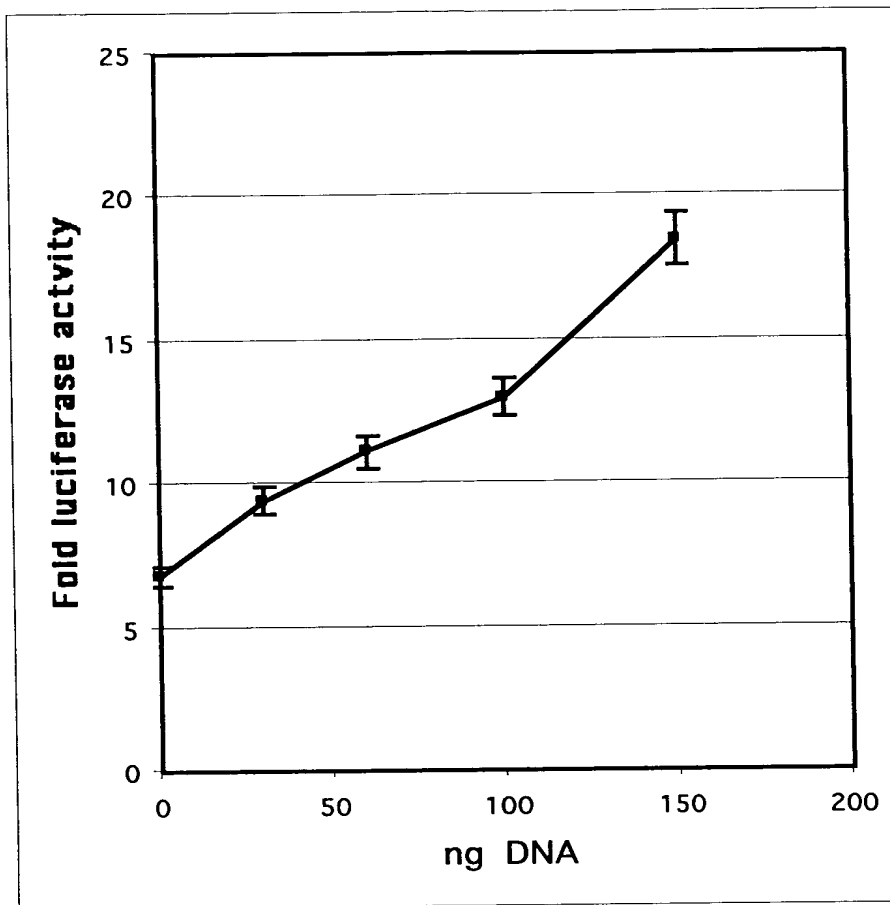
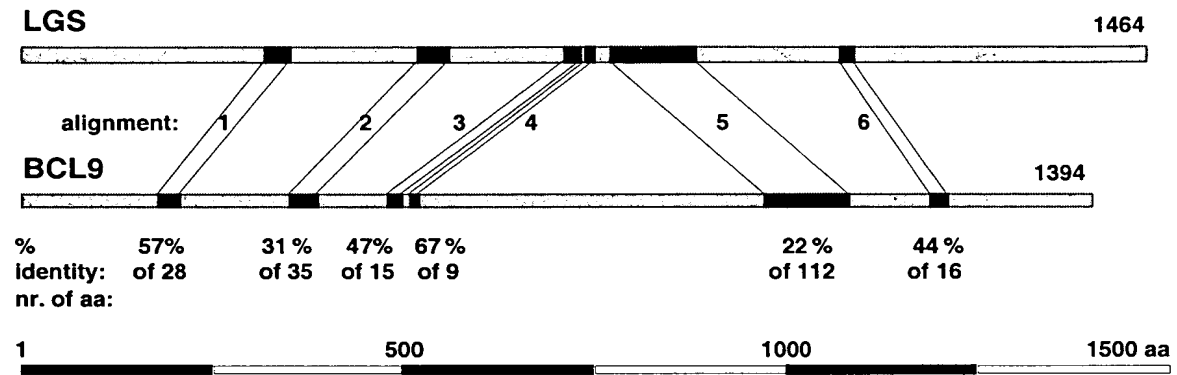


Figure 7

A



7B

Sequence homology domain 1: 57.1% identity in 28 aa

	320	330	340
LGS	IFVFSTQLANKGAESVLSGQFQTIIAYH		
	::
BCL9	VYVFSTEMANKAAEAVLKGQVETIVSFH		
	180	190	200

Sequence homology domain 2: 31.4% identity in 35 aa

	520	530	540
LGS	ENLTPQQRQHREBQLAKIKKMNQFLFPENENSVGA		

BCL9	DGLSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGA		
	350	360	370 380

Sequence homology domain 3: 46.7% identity in 15 aa

	710	720
LGS	QMEWSKIQHQFFEER	
	
BCL9	QIAWLKLQQEFYEEK	
	470	480

Sequence homology domain 4: 66.6% identity in 9 aa

	760
LGS	LQGPPPPYH

BCL9	VRGPPPPYQ
	520

Sequence homology domain 5: 22.3% identity in 112 aa

	770	780	790	800	810	820
LGS	SASVPIATQSPNPSSPNNLSLPSRPTTAAVMGLPTNSPSMDGTGSLSGSVPQANTSTVQA					

BCL9	GPPPTASQPASVNI PGSLSSTPYTMPPEPTLSQNPLSIM-MSRMSKFAMPSSSTPLYHD					
	970	980	990	1000	1010	1020
	830	840	850	860	870	
LGS	GTTTVLSANKNCFQADTPSPSNQNRSRNTGSSSVLTHNLSSNPSTPLSHLSP					
	.. :: :.. .	:: :.. .	: : :.. .	: : :.. .	: : :.. .	: : :.. .
BCL9	AIKTVASSDDSPPARSPNLPSMNNMPGMGINTQNPRISGPNPVVPMPTLSP					
	1030	1040	1050	1060	1070	

Sequence homology domain 6: 43.8% identity in 16 aa

	1080
LGS	NPKMCVAGGPNGPPGF
	.. :: :.. .
BCL9	DAALCKPGGPGGPDSE
	1190 1200

Figure 8

A

ATGCATTCCAGTAACCCCTAAAGTGAGGAGCTCTCCATCAGGAAACACACA
GAGTAGCCCTAAGTCAAAGCAGGAGGTGATGGTCCGTCCCCCTACAGTGA
TGTCCTCCATCTGGAACCCCCAGCTGGATTCCAAATTCTCCAATCAGGGT
AAACAGGGGGGGCTCAGCCAGCCAATCCCAGCCATCCCCCTGTGACTCCAA
GAGTGGGGGGCCATACCCCCTAAAGCACTCCCTGGCCCAGGTGGGAGCATGG
GGCTGAAGAATGGGGCTGGAAATGGTGCCAAGGGGCAAGGGGAAAAGGGAG
CGAAGTATTTCCGCCGACTCCTTTGATCAGAGAGATCCTGGGACTCCAAA
CGATGACTCTGACATTAAAGAATGTAATTCTGCTGACCACATAAAGTCCC
AGGATTCCCAGCACACACCACACTCGATGACCCCATCAAATGCTACAGCC
CCCAGGTCTTCTACCCCCCTCCCATGGCCAACTACTGCCACAGACCCCAC
ACCTGCTCAGAAGACTCCAGCCAAAGTGGTGTACGTGTTTTCTACTGAGA
TGGCCAATAAAGCTGCAGAAGCTGTTTTGAAGGGCCAGGTTGAACTATC
GTCTCTTTCCACATCCAGAACATTTCTAACAACAAGACAGAGAGAAGCAC
AGCGCCTCTGAACACACAGATATCTGCCCTTCGGAATGATCCGAAACCTC
TCCCACAACAGCCCCCAGCTCCGGCCAACCAGGACCAGAATTCTTCCAG
AATACCAGACTGCAGCCAACTCCACCCATTCCGGCACCAGCACCCAAGCC
TGCCGCACCCCCACGTCCCTGGACCGGGAGAGTCCTGGGGTAGAAAACA
AACTGATTCTTCTGTAGGAAGTCCTGCCAGCTCCACTCCACTGCCCCCA
GATGGTACTGGGCCCCAACTCAACTCCCAACAATAGGGCAGTGACCCCTGT
CTCCCAGGGGAGCAATAGCTCTTCAGCAGATCCCAAAGCCCCCTCCGCTC
CACCAGTGTCCAGTGGCGAGCCCCCACAACACTGGGAGAGAATCCCGATGGC
CTATCTCAGGAGCAGCTGGAGCACCGGGAGCGCTCCTTACAACTCTCAG
AGATATCCAGCGCATGCTTTTTCTGATGAGAAAGAATTCACAGGAGCAC
AAAGTGGGGGACCGCAGCAGAATCCTGGGGTATTAGATGGGCCTCAGAAA
AAACCAGAAGGGCCAATACAGGCCATGATGGCCCAATCCCAAAGCCTAGG
TAAGGGACCTGGGGCCCCGGACAGACGTGGGAGCTCCATTTGGCCCTCAAG
GACATAGAGATGTACCCTTTTTCTCCAGATGAAATGGTTCCACCTTCTATG
AACTCCCAGTCTGGGACCATAGGACCCGACCACCTTGACCATATGACTCC
CGAGCAGATAGCGTGGCTGAAACTGCAGCAGGAGTTTTATGAAGAGAAGA
GGAGGAAGCAGGAACAAGTGGTTGTCCAGCAGTGTTCCCTCCAGGACATG
ATGGTCCATCAGCACGGGCCTCGGGGAGTGGTCCGAGGACCCCCCCCCCTOC
ATACCAGATGACCCCTAGTGAAGGCTGGGCACCTGGGGGTACAGAGCCAT
TTTCTGATGGTATCAACATGCCACATTCTCTGCCCCCGAGGGGCATGGCT
CCCCACCCCAACATGCCAGGGAGCCAGATGCGCCTCCCTGGATTTGCAGG
CATGATAAACTCTGAAATGGAAGGGCCGAATGTCCCCAACCCTGCATCTA
GACCAGGTCTTTCTGGAGTCAGTTGGCCAGATGATGTGCCAAAAATCCCA
GATGGTCGAAATTTTCTCCTGGCCAGGGCATTTCAGCGGTCTTGCCG
AGGGGAACGCTTCCCAAACCCCCAAGGATTGTCTGAAGAGATGTTTCAGC
AGCAGCTGGCAGAGAAACAGCTGGGTCTCCCCCAGGGATGGCCATGGAA
GGCATCAGGCCCAGCATGGAGATGAACAGGATGATTCAGGCTCCAGCG
CCACATGGAGCCTGGGAATAACCCCATTTTCCCTCGAATACCAGTTGAGG
GCCCTCTGAGTCCTTCTAGGGGTGACTTTCCAAAAGGAATTCCCCCACAG

Figure 8A

ATGGGCOOCTGGTTCGGGAACCTTGAGTTTGGGATGGTTCTAGTGGGATGAA
GGGAGATGTCAATCTAAATGTCAACATGGGATCCAACTCTCAGATGATAC
CTCAGAAGATGAGAGAGGCTGGGGCGGGCCCTGAGGAGATGCTGAAATTA
CGCCCAGGTGGCTCAGACATGCTGCCTGCTCAGCAGAAGATGGTGCCACT
GCCATTTGGTGAGCACCCCCAGCAGGAGTATGGCATGGGCCCCAGACCAT
TCCTTCCCATGTCTCAGGGTCCAGGCAGCAACAGTGGCTTGCGGAATCTC
AGAGAACCAATTGGGCCCCGACCAGAGGACTAACAGCCGGCTCAGTCATAT
GCCACCACTACCTCTCAACCCTTCCAGTAACCCACCAGCCTCAACACAG
CTCCTCCAGTTCAGCGCGGCCTGGGGCGGAAGCCCTTGATATATCTGTG
GCAGGCAGCCAGGTGCATTCCCCAGGCATTAACCCCTCTGAAGTCTCCAC
GATGCACCAAGTCCAGTCACCAATGCTGGGCTCGCCCTCGGGGAACCTCA
AGTCCCCCAGACTCCATCGCAGCTGGCAGGCATGCTGGCGGGGCCAGCT
GCTGCTGCTTCCATTAAGTCCCCCCTGTTTTGGGGTCTGCTGCTGCTTC
ACCTGTCCACCTCAAGTCTCCATCACTTCCTGCCCCGTACCTGGATGGA
CCTCTTCTCCAAAACCTCCCCTTCAGAGTCCTGGGATCCCTCCAAACCAT
AAAGCACCCCTCACCATGGCCTCCCCAGCCATGCTGGGAAATGTAGAGTC
AGGTGGCCCCCACCTCCTACAGCCAGCCAGCCTGCCTCTGTGAATATCC
CTGGAAGTCTTCCCTCTAGTACACCTTATACCATGCCTCCAGAGCCAACC
CTTTCCCAGAACCCACTCTCTATTATGATGTCTCGAATGTCCAAGTTTGC
AATGCCCAGTTCCACCCCGTTATACCATGATGCTATCAAGACTGTGGCCA
GCTCAGATGACGACTCCCCTCCAGCTCGTTCTCCCAACTTGCCATCAATG
AATAATATGCCAGGAATGGGCATTAATACACAGAATCCTCGAATTTCAGG
TCCAAACCCCGTGGTTCCGATGCCAACCCCTCAGCCCAATGGGAATGACCC
AGCCACTTTCTCACTCCAATCAGATGCCCTCTCCAAATGCCGTGGGACCC
AACATACCTCCTCATGGGGTCCCAATGGGGCCTGGCTTGATGTCACACAA
TCCTATCATGGGGCATGGGTCCCAGGAGCCACCGATGGTACCTCAAGGAC
GGATGGGCTTCCCCCAGGGCTTCCCTCCAGTACAGTCTCCCCACAGCAG
GTTCCATTCCCTCACAATGGCCCCAGTGGGGGGCAGGGCAGCTTCCCAGG
AGGGATGGGTTTCCCAGGAGAAGGCCCCCTTGCCCGCCCCAGCAACCTGC
CCCAAAGTTCAGCAGATGCAGCACTTTGCAAGCCTGGAGGCCCCGGGGGT
CCTGACTCCTTCACTGTCCTGGGGAACAGCATGCCTTCGGTGTTTACAGA
CCCAGATCTGCAGGAGGTATCCGACCTGGAGCCACCGGAATACCTGAGT
TTGATCTATCCCGCATTATTCCATCTGAGAAGCCCAGCCAGACGCTGCAA
TATTTCCCTCGAGGGGAAGTTCCAGGCCGTAAACAGCCCCAGGGTCTGG
ACCTGGGTTTTTACACATGCAGGGGATGATGGGCGAACAAGCCCCCAGAA
TGGGACTAGCATTACCTGGCATGGGAGGTCCAGGGCCAGTGGGAACTCCG
GACATCCCTCTTGGTACAGCTCCATCCATGCCAGGCCACAACCCCATGAG
ACCACCAGCCTTTCTCCAACAAGGCATGATGGGACCTCACCATCGGATGA
TGTCACCAGCACAATCTACAATGCCCGGCCAGCCCACCCTGATGAGCAAT
CCAGCTGCTGCCGTGGGCATGATTOCTGGCAAGGATCGGGGGCCTGCCGG
GCTCTACACCCACCCTGGGCCTGTGGGCTCTCCAGGCATGATGATGTCCA
TGCAGGGCATGATGGGACCCCAACAGAACATCATGATCCCCCAGAGATG
AGGCCCCGGGGCATGGCTGCTGACGTGGGCATGGGTGGATTTAGCCAAGG
ACCTGGCAACCCAGGAAACATGATGTTTTAA

Figure 8B

B

MHSSNPKVRSSPSGNTQSSPKSKQEVMMVRPPTVMSPSGNPQLDSKFSNQG
KQGGASASQSPSPCDKSGGHTPKALPGPGGSMGLKNGAGNGAKGKGKRE
RSISADSFQDRDPGTPNDDSDIKECNSADHIKSQDSQHTPHSMTPSNATA
PRSTPSHGQTTATEPTPAQKTPAKVVYVFSTEMANKAAEAVLKQVETI
VSFHIQNISNNKTERSTAPLNTQISALRNDPKPLPQQPPAPANQDQNSSQ
NTRLQPTPIPAAPAPKPAAPPRPLDRESPGVENKLIPSVGSPASSTPLPP
DGTGPNSTPNRAVTPVSQGSNSSSADPKAPPPPPVSSGEPPTLGENPDG
LSQEQLHRERSLQTLRDIQRMFLPDEKEFTGAQSGGPQQNPGVLDGPQK
KPEGPIQAMMAQSQSLGKGPGRPTDVGAPFGPQGHVDVPFSPDEM/PPSM
NSQSGTIGPDHLDHMTPEQIAWLKQQEFYEEKRRKQEQVVVQQCSLQDM
MVHQHGPRGVVRGPPPPYQMTPEGWAPGGTEPFSDGINMPHSLPPRGMA
PHPNMPGSQMRLPGFAGMINSEMEGPNVNPASRPGLSGVSWPDDVPKIP
DGRNFPFGQGIFSGPGRGERFPNPQGLSEEMFQQQLAEKQLGLPPGMAME
GIRPSMEMNRMIPGSQRHMEPGNNPIFPRIPEGPLSPSRGDFPKGIPPO
MGPGRELEFGMVPSGMKGDVNLNVNMGNSNSQMIPQKMREAGAGPEEMLKL
RPGGSDMLPAQQKMVPLPFGEHPQQEYGMGPRPFLPMSQGPGSNSGLRNL
REPIGPDQRTNSRLSHMPPLPLNPSSNPTSNTAPPVQRGLGRKPLDISV
AGSQVHSPGINPLKSPTMHQVQSPMLGSPSGNLKSPQTPSQLAGMLAGPA
AAASIKSPPVLGSAASPVLKSPSLPAPSPGWTSSPKPPLQSPGIPPNH
KAPLTMASPAMLGNVESGGPPPPTASQPASVNIPGSLPSSTPYTMPPEPT
LSQNPLSIMMSRMSKFAMPSSTPLYHDAIKTVASSDDDSPPARSPNLPSM
NNMPGMG!NTQNPRISGPNPVVPMPTLSPMGMGTQPLSHSNQMPSPNAVGP
NIPPHGVPMGPGLMSHNPIMGHGSQEPPMVPOGRMGFPQGFPPVQSPPOQ
VPFPHNGPSGGQGSFPFGMGFPGEGLGRPSNLPQSSADAALCKPGGPGG
PDSFTVLGNSMPSVFTDPDLQEVIRPGATGIPEFDLSRIIPSEKPSQTLQ
YFPRGEVPGRKQPQGPFGFSHMQGMMGEQAPRMGLALPGMGGPGPVGTP
DIPLGTAPSMPGHNPMRPPAFLQQGMMGPHHRMMSPAQSTMPGQPTLMSN
PAAAVGMIPGKDRGPAGLYTHPGPVGSPGMMMSMQGMMGPQQNIMIPPQM
RPRGMAADVGMGGFSQGPGNPGNMMF*

Figure 9

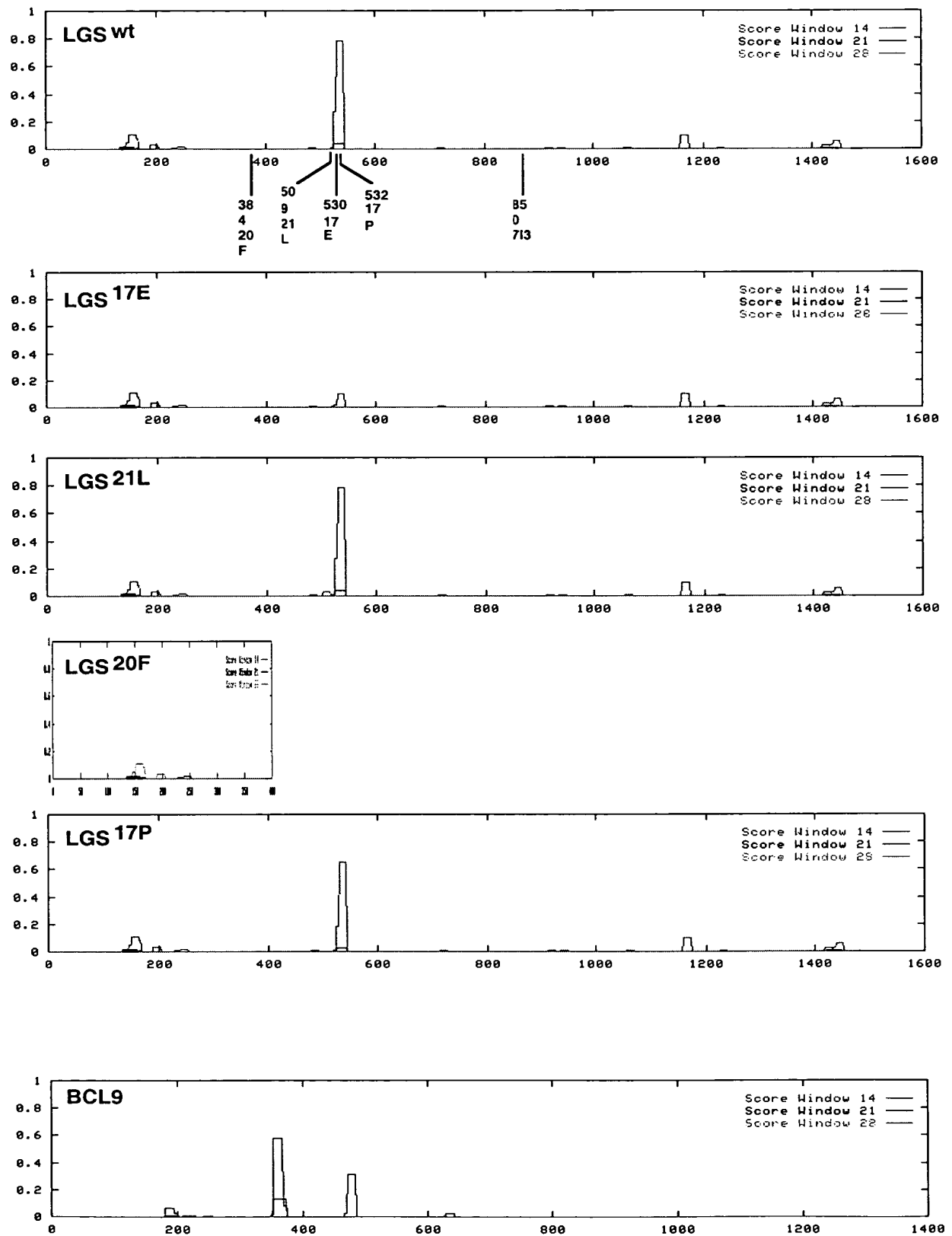


Figure 10

A

ATGGCCTGCTTCCCATCCCCTGCTGCCATCTCCTGCACCCTTAGGGCACAGTGGGCATCT
CGGGAGCTGCTCAGCGGACAGACTAGGGTTACCCCCACCCCAGGAGGAGAGAAAGCTCCAG
GGAGCCCGCGTGTCCCCCGGGTCATTGCCCCCTGCCCCAGCCAAGCCAATGCACCCA
GAAAATAAATTGACCAATCATGGCAAGACAGGGAATGGCGGGGGCCCAATCTCAGCACCAG
AATGTGAACCAAGGACCCACCTGCAACGTGGGCTCGAAGGGCGTGGGGGCGGGGAACCAT
GGGGCCAAGGCCAACCAGATCTCGCCTAGCAACTCAAGTCTGAAGAACCCCCAGGCAGGG
GTGCCCCCTTTTCAGCTCGCTCAAGGGCAAGGTGAAGAGGGACCGGAGTGTGTCTGTGGAC
TCTGGAGAGCAGCGAGAGGCTGGGACCCCATCCCTGGATTTCAGAGGCCAAAGAGGTGGCG
CCGCGGAGTAAGCGGCGCTGTGTGCTGGAGCGGAAGCAGCCGTACAGTGGGGACGAATGG
TGCTCTGGACCGACAGTGAAGGAGACGACAAGCCCATTGGGGGCCACCCACAAAGCTGCT
TTCAAAGAAGACGGCTTTTCAGGACAAGGCATCACACTTCTTCTCCAGCACGTACAGTCTT
GAAACCTCCAGGAGGAAGCTGCCCCAAGCCCCGAAGGCTTCCTTCCTGGGGCAGCAGGGC
CGAGTCATTTGGAAACCTCTCTCGGAGGAGCTCCGTGATCAAGGTGCAGATGCGGCAGGT
GGGCGGGCCTCAATCATGTCTCCAATCGCGACGGTGAATGCGAGTGGCTTGTCCAAAGAG
CAGCTGGAGCATCGGGAACGGTCCCTCCAGACGCTGCGAGACATTGAGCGACTGCTGCTC
CGCAGCGGAGAGACTGAGCCCTTCCTCAAGGGGGCCCCCAGGAGGAGCGGCGGGCTGAAG
AAATATGAGGAACCTTTCAGTCCATGATTTTACAGACACAGAGCCTAGGGGGGCCCCCG
CTGGAGCATGAAGTGCCTGGGCACCCCCCGGGTGGGGACATGGGGCAGCAGATGAACATG
ATGATACAGAGGCTGGGCCAGGACAGCCTCACGCCTGAGCAGGTGGCCTGGCGCAAGCTG
CAGGAGGAGTACTACGAAGAGAAACGGCGGAAAGAGGAACAGATTGGGCTGCATGGGAGC
CGTCTCTGCGAGGACATGATGGGCATGGGGGGCATGATGGTGAAGGGGGCCCCCGCCTCCT
TACCACAGCAAGCCTGGGGATCAGTGGCCACCTGGAATGGGTGCGCAGCTGCGGGGGCCC
ATGGATGTTCAAGATCCCATGCAGTCCGGGGCGGACCTCCCTTTCCTGGGCCCCGTTTC
CCAGGCAACCGACATACAACGGGTACCTGGGTTTGGGGGCATGCGAGATATGCCCATGGAG
GTGCCCATGAATGCCATGCAGAGGCCCGTGAGACCAGGCATGGGCTGGACCGAAGACTTG
CCCCCTATGGGGGGACCCAGCAATTTTGGCCAGAACACCATGCCCTACCCAGGTGGGCAG
GGTGAGGCGGAGCGATTTCATGACTCCCCGGGTCCGTGAGGAGCTGCTGCGGCACCAGCTG
CTGGAGAAGCGGTTCGATGGGCATGCAGCGCCCCCTGGGCATGGCAGGCAGTGGCATGGGA
CAGAGCATGGAGATGGAGCGGATGATGCAGGCGCACCGACAGATGGATCCTGCCATGTTT
CCCCGGCAGATGGCTGGTGGTGAGGGCCTGGCGGGCACTCCCATGGGCATGGAGTTTGGT
GGAGGCCGGGGCCTCCTGAGCCCTCCCATGGGGCAGTCTGGGCTGAGGGAGGTGGACCCA
CCCATGGGGCCAGGCAACCTCAACATGAACATGAATGTCAACATGAACATGAACATGAAC
CTGAACGTGCAGATGACCCCGCAGCAGCAGATGCTGATGTGCGAGAAGATGCGGGGCCCT
GGGGACTTGATGGGGCCCCAGGGCCTCAGTCTGAGGAGATGGCCCGGGTTCGGGGCCAG
AACAGCAGTGGCATGGTGCCCTTGCCCTTCTGCCAACCCGCCAGGACCTCTCAAGTCGCCC
CAGGTCCCTCGGCTCCTCCCTCAGTGTCCGTTACCCACTGGCTCGCCCAGCAGGCTCAAG
TCTCCTTCCATGGCGGTGCCTTCTCCAGGTGGGTTGCCTCACCCAAGACGGCCATGCC
AGCCCCGGGGTCTCCCAAGAACAGCAGCCGCTCTCAACATGAACCTCTCCACCACCTG
AGCAACATGGAACAGGACCCACACCTTCCCAGAACCCCCCTGTCACTGATGATGACCCAG
ATGTCCAAGTACGCCATGCCAGCTCCACCCGCTCTACCACAATGCCATCAAGACCATC
GCCACCTCAGACGACGAGCTGCTGCCCCGACCGGCCCTGCTGCCCCCCCCACCCTCCACCG
CAGGGCTCCGGGCCAGGTGGCCCCGACTCCCTGAATGCCCCCTGTGGCCAGTGGCCAGC
TCCTCCCAGATGATGCCCTTCCCCCTCGGCTGCAGCAGCCCCATGGTGCCATGGCCCCC
ACTGGGGGTGGGGGCGGGGGCCTGGCCTGCAGCAGCACTACCCGTGAGGCATGGCCCTG
CCTCCCGAGGACCTGCCCAACCAGCCGCCAGGCCCCATGCCTCCCCAGCAGCACCTGATG
GGCAAAGCCATGGCTGGGCGCATGGGCGACGCATACCCACCGGGTGTGCTCCCTGGGGTG
GCATCAGTGCTGAACGACCCCGAGCTGAGCGAGGTGATCCGGGCCACCCCAACGGGGATC
CCCGAGTTGCACTTGTGAGGATCATCCCCTCTGAGAAGCCAAGCAGCACCCCTCCAGTAC
TTCCCCAAGAGCGAGAACCAGCCCCCAAGGCTCAGCCCCCTAATCTGCATCTCATGAAC
CTGCAAGACTGAGCGGAGCAGACTCCCTCTCGGCCTCCCAACCTCCCAGGCCAGCAG
GGCGATCGGCGCTGGTGGTGATACCGGGTACCCGGGCTATGGCGCCGGCGCAGCGC
TGCCCTCTGTGCCGCCAGACCTTCTTCTGTGGTTCGCGGGCACGTTTACAGCCGCAAGCAC
CAGCGGCAGCTGAAGGAGGCTTTGGAGAGGCTCCTGCCCCAGGTGGAGGCGGGCCGCAAG
GCCATCCGCGCCGCTCAGGTGGAGCGCTATGTGCCGAACACGAGCGATGCTGCTGGTGC
CTGTGCTGCGGCTGTGAGGTGCGGGAACACCTGAGCCATGGAAACCTGACGGTGTGTAC

Figure 10

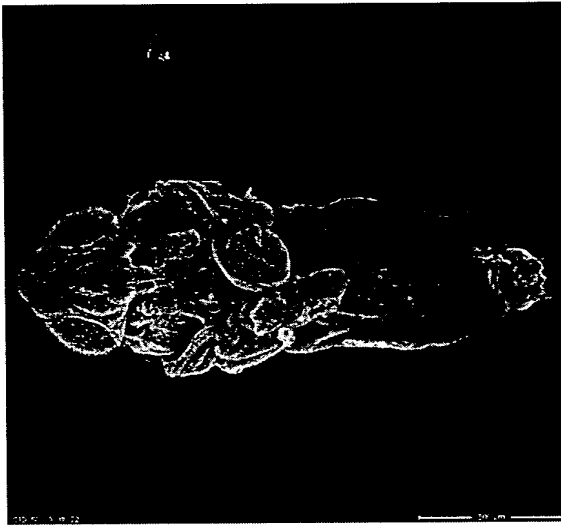
GGGGGGCTGCTGGAGCATCTGGCCAGCCCAGAGCACAAGAAAGCAACCAACAAATTCTGG
TGGGAGAACAAAGCTGAGGTCCAGATGAAAGAGAAGTTTCTGGTCACTCCCCAGGATTAT
GCGCGATTCAAGAAATCCATGGTGAAAGGTTTGGATTCTATGAAGAAAAGGAGGATAAA
GTGATCAAGGAGATGGCAGCTCAGATCCGTGAGGTGGAGCAGAGCCGACAGGAGGTGGTT
CGGTCTGTCTTAGAGACAGGTCCCCCAAGATACGCCCTCACAGTCCGGTCCCCCGCCGTC
CTCTCCCGGCGCACGCTCAAGTCCGGTGCCTTCCCCCGCAGACCCCCGAGGCGCACCCCT
CAAGCTCGGTGCCTCTGCGCCCCCGCAGGGGCGCCCTCAAGCCTGAGCCCCCGGGCGC
ACCCTCAAGCTCGGTGTACCCCCCATACACCCGCAAGGCGCGCCCTCATGCCGCGAAG
ACTTCGCCCCGCCAAGGTGCACCCGTCAAGCCCCGAATAAAACCCAGTCACTCCAACCTT
GCAGGCAAAGCTAGAAAACTGCGCTGCATTTGCAAACAAAAGCTCTTGTTGGCGATGAC
GATACTGTTTTGGGTGTGAAACTGTCAATTGCTAACTACGATCTGTGA

B

FKEDGFQDKASHFFSSTYSPETSRRKLPQAPKASFLGQQGRVIWKPLSEE
LRDQGADAAGGPASIMSPIATVNASGLSKEQLEHRERSLQTLRDIERLLL
RSGETEPFLKGAPRRSGGLKKYEEPLQSMISQTQSLGGPPLEHEVPGHPP
GGDMGQQMNMIMQRLGQDSLTPQVAVWRKLQEEYEEKRRKEEQIGLHGS
RPLQDMMGMGGMVVRGPPPPYHSPKPGDQWPPGMGAQLRGPMDVQDPMQLR
GGPPFPGRFPGNQIQRVPGFGGMQSMPMEVPMNAMQRPVRPGMGWTEDL
PPMGGPSNFAQNTMPYPGGQGEAERFMTPRVREELLRHQLLEKRSMGMQR
PLGMAGSGMGQSMEMERMMQAHQMDPAMFPGQMAGGEGLAGTPMGMEFG
GGRGLLSPPMGQSGLEVDPPMGPGNLMNMNMVNMNMNMNLNVQMTPQQQ
MLMSQKMRGPGDLMGPQGLSPEEMARVRAQNSSGMVPLPSANPPGPLKSP
QVLGSSLSVRSPTGSPSRLKSPSMAVPSPGWVASPKTAMPSPGVSQNKQP
PLNMNSSTTLNMEQDPTPSQNPLSLMMTQMSKYAMPSSTPLYHNAIKTI
ATSDDELLPDRPLPPPPPPQSGPGGPDNLNAPCGVPVSSSQMMPFPPR
LQQPHGAMAPTGGGGGGPGLQQHYPSGMALPPEDLPNQPPGPMPPQQHLM
GKAMAGRMGDAYPPGVLPGVASVLNDPELSEVIRPTPTGIPEFDLSRIIP
SEKPSSTLQYFPKSENQPPKAQPPNLHLMNLQNMMAEQTPSRPPNLPQQQ
GDRPLVWVIPGTRAMAPAQRCLCRQTFFCGRGHVYSRKHQRQLKEALER
LLPQVEAARKAIRAAQVERYVPEHERCCWCLCCGCEVREHLSHGNLTVLY
GGLEHLASPEHKKATNKFWWENKAEVQMKEKFLVTPQDYARFKKSMVKG
LDSYEEKEDKVIKEMAAQIREVEQSRQEVRSVLETGPPRYALTVRSPAV
LSRRTLKSGAFPPQTPEAHPQARCLCAPRRGALKPEPPGRTLKLGVPPTH
TRKARPHAAKTSPRPRCTRQAPNKTQSLQLAGKARKTALHLQTKALVGDD
DTVLGVKLSIANYDL

Figure 11

A



B



Figure 12

A

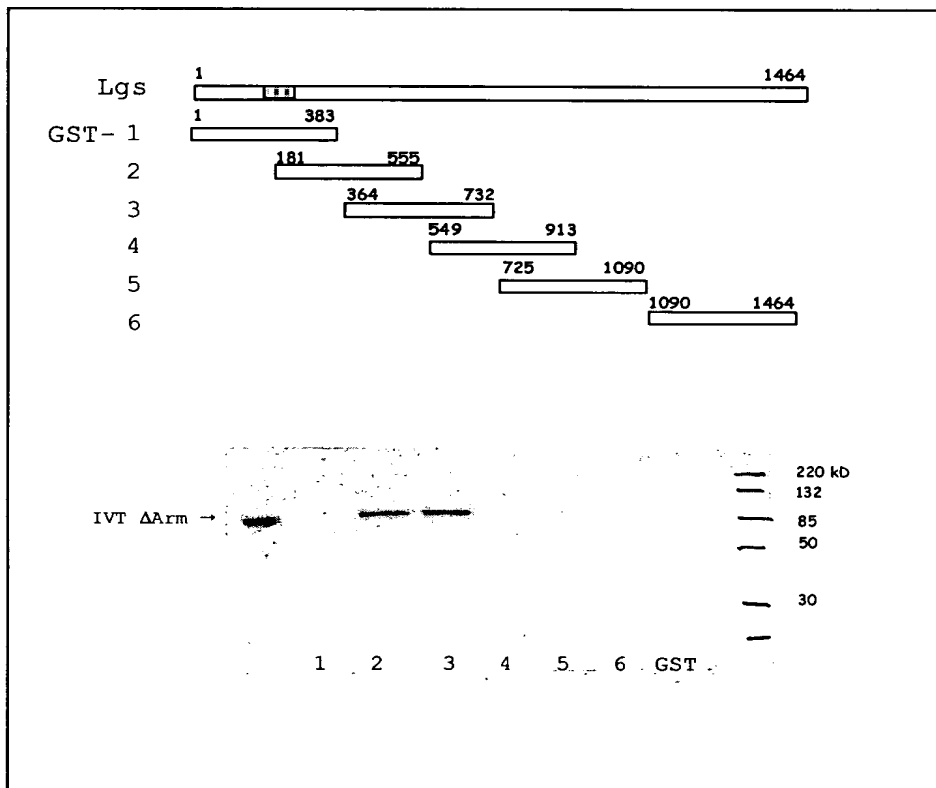
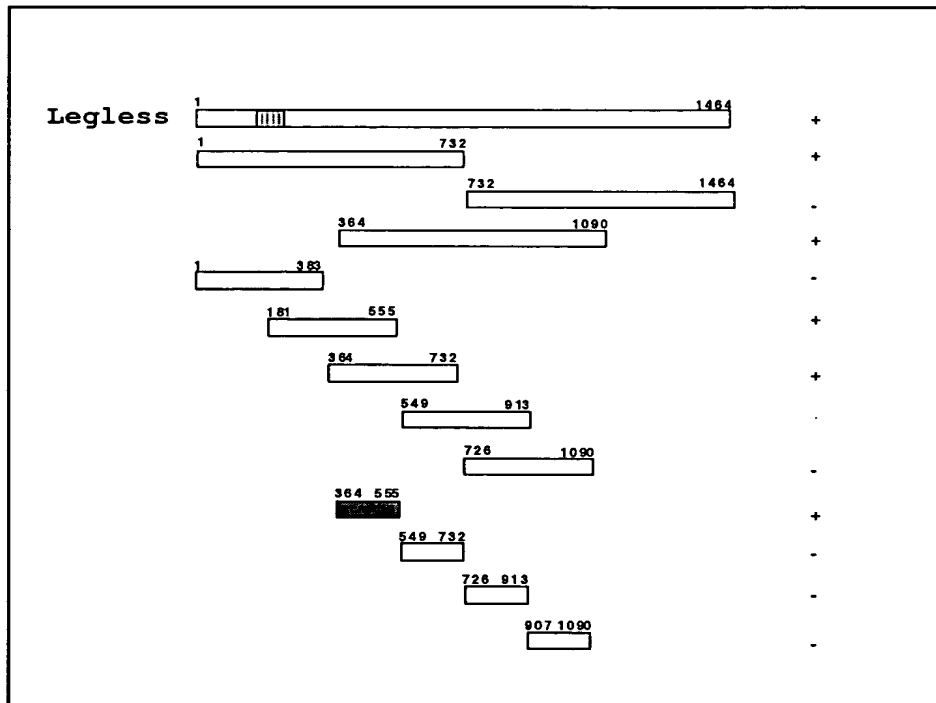


Figure 12B

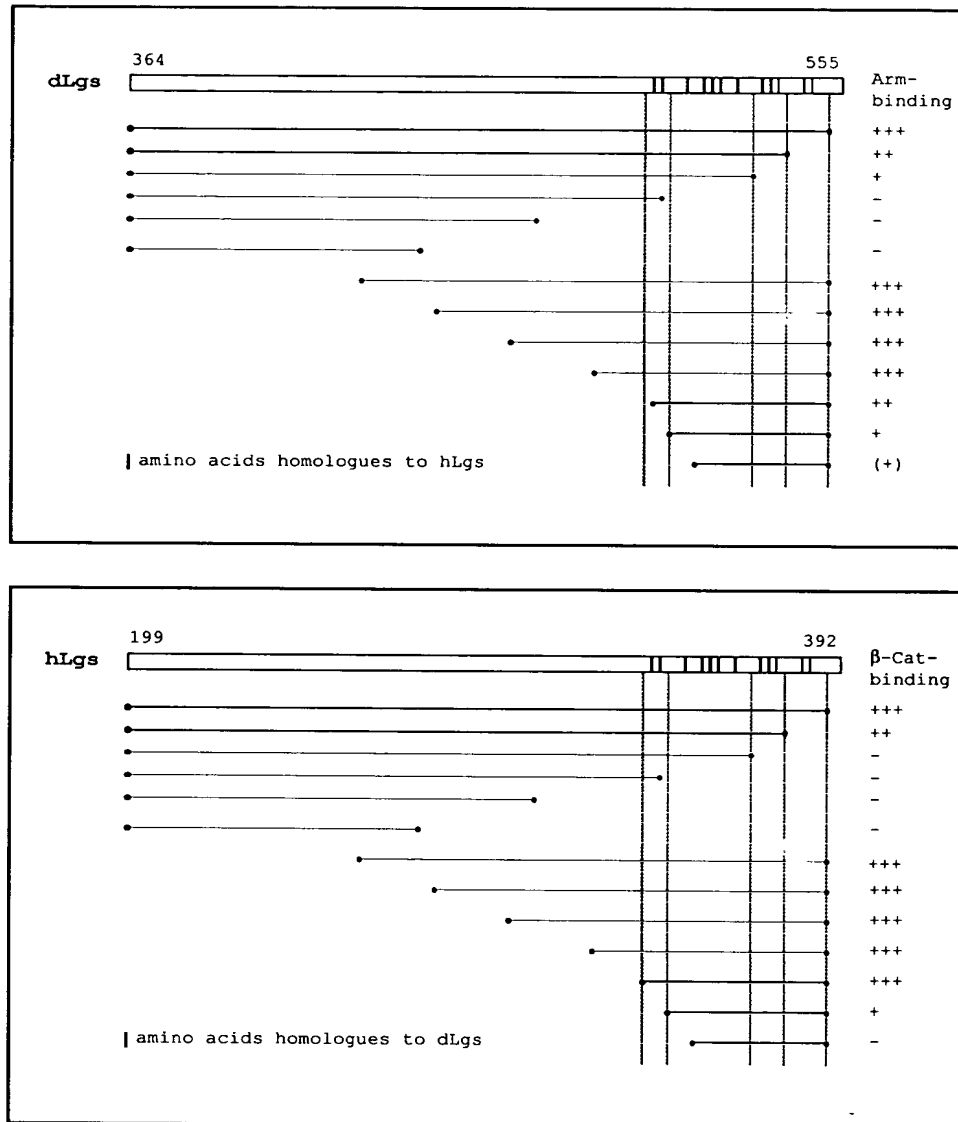


Figure 12C










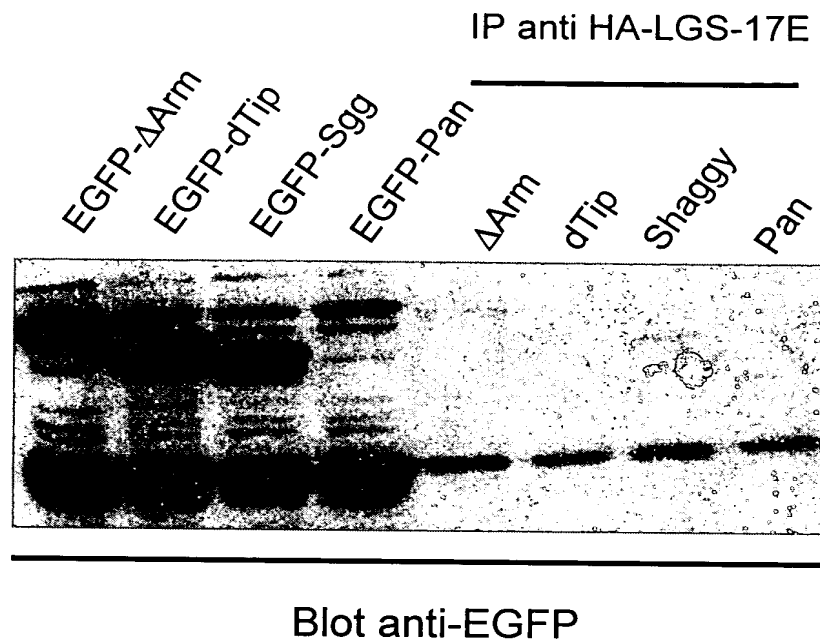
	In vitro interaction
N  1 2 3 4 5 6 7 8 9 10 11 12 13  C	++
1 2 3 4 5 6 7 8 9 10 11 12 13  C	++
 C	-
N  1 2 3 4 5 6 7 8 9 10 11 12 13	++
N  1 2 3 4 5 6 7 8	+++
N  1 2 3 4 5 6	+++
N  1 2 3 4	++
N  1 2	-
1 2 3 4 5 6 7 8 9 10 11 12 13	++
1 2 3 4 5 6 7 8	+++
1 2 3 4 5 6	+++
1 2 3 4	++
1 2	-
3 4 5 6 7 8	(+)
5 6 7 8	(-)
7 8 9 10 11 12 13	(-)
9 10 11 12 13	(-)

Figure 13

A



B

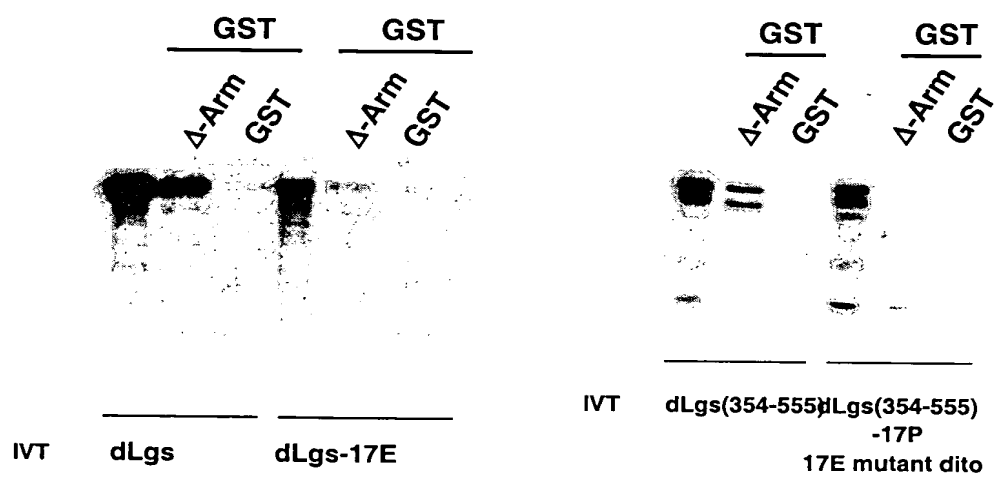
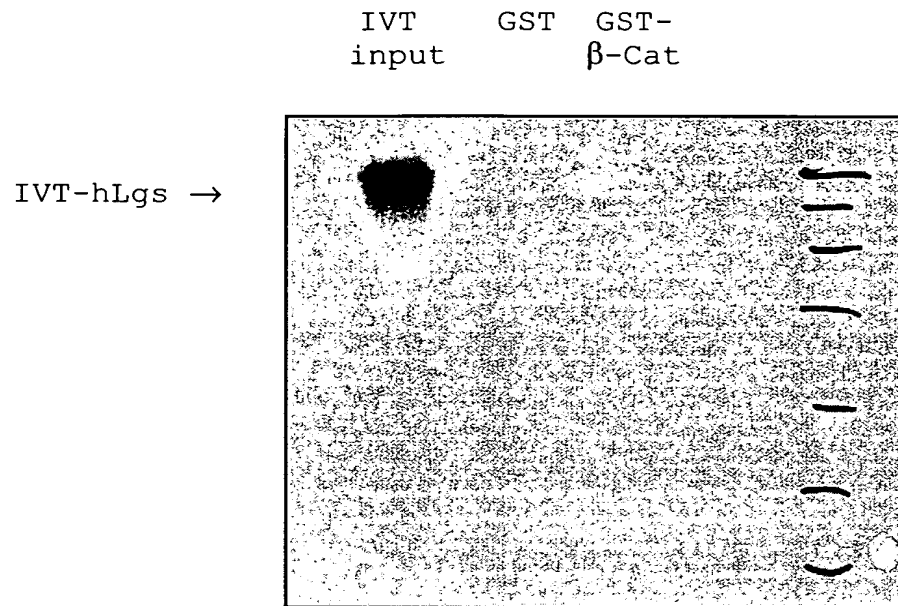


Figure 13

C



D

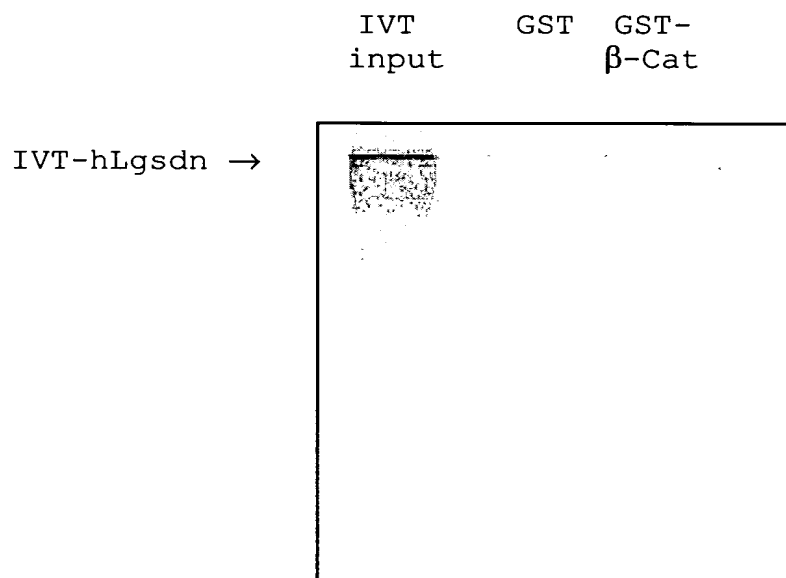


Figure 14

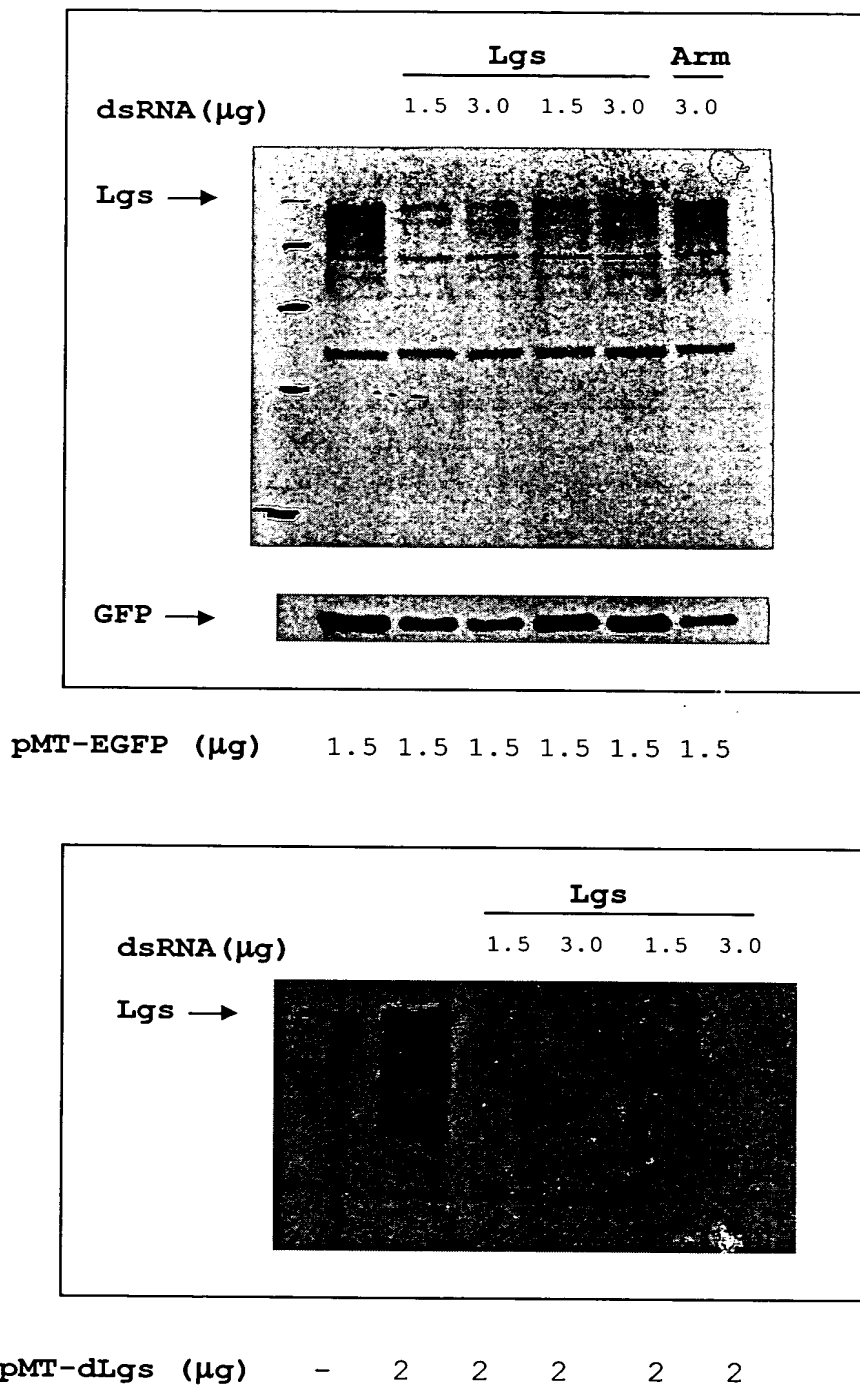
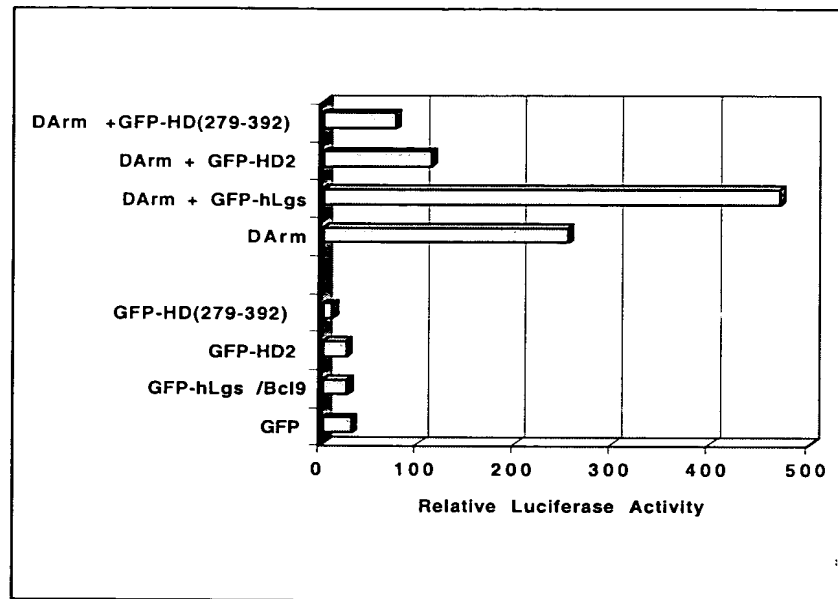


Figure 15

A



B

